

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/116,676

DATE: 07/21/98  
TIME: 14:20:11

INPUT SET: S27568.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

- 1
- 2
- 3 (1) General Information:
- 4
- 5 (i) APPLICANT: Borowsky, Beth
- 6
- 7 (ii) TITLE OF INVENTION: DNA ENCODING A HUMAN Ob RECEPTOR
- 8 (hOb-Re) AND USES THEREOF
- 9
- 10 (iii) NUMBER OF SEQUENCES: 29
- 11
- 12 (iv) CORRESPONDENCE ADDRESS:
- 13 (A) ADDRESSEE: Cooper & Dunham LLP
- 14 (B) STREET: 1185 Avenue of the Americas
- 15 (C) CITY: New York
- 16 (D) STATE: New York
- 17 (E) COUNTRY: USA
- 18 (F) ZIP: 10036
- 19
- 20 (v) COMPUTER READABLE FORM:
- 21 (A) MEDIUM TYPE: Floppy disk
- 22 (B) COMPUTER: IBM PC compatible
- 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 25
- 26 (vi) CURRENT APPLICATION DATA:
- 27 (A) APPLICATION NUMBER:
- 28 (B) FILING DATE:
- 29 (C) CLASSIFICATION:
- 30
- 31 (viii) ATTORNEY/AGENT INFORMATION:
- 32 (A) NAME: White, John P
- 33 (B) REGISTRATION NUMBER: 28,678
- 34 (C) REFERENCE/DOCKET NUMBER: 1795-53801/JPW/KDB
- 35
- 36 (ix) TELECOMMUNICATION INFORMATION:
- 37 (A) TELEPHONE: 212 278 0400
- 38 (B) TELEFAX: 212 291 0525
- 39
- 40
- 41 (2) INFORMATION FOR SEQ ID NO:1:
- 42
- 43 (i) SEQUENCE CHARACTERISTICS:
- 44 (A) LENGTH: 54 base pairs
- 45 (B) TYPE: nucleic acid
- 46 (C) STRANDEDNESS: single

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47 (D) TOPOLOGY: linear  
48  
49 (ii) MOLECULE TYPE: DNA  
50  
51 (ix) FEATURE:  
52 (A) NAME/KEY: CDS  
53 (B) LOCATION: 1..54  
54  
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
56  
57 AAT GTT AAA AAG TTT CAC ATC CAC GGT ATG TGT ACT GTA CTT TTC ATG 48  
58 Asn Val Lys Lys Phe His Ile His Gly Met Cys Thr Val Leu Phe Met  
59 1 5 10 15  
60  
61 GAT TAG 54  
62 Asp \*  
63  
64  
65  
66 (2) INFORMATION FOR SEQ ID NO:2:  
67  
68 (i) SEQUENCE CHARACTERISTICS:  
69 (A) LENGTH: 17 amino acids  
70 (B) TYPE: amino acid  
71 (D) TOPOLOGY: linear  
72  
73 (ii) MOLECULE TYPE: protein  
74  
75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
76  
77 Asn Val Lys Lys Phe His Ile His Gly Met Cys Thr Val Leu Phe Met  
78 1 5 10 15  
79  
80 Asp  
81  
82  
83  
84 (2) INFORMATION FOR SEQ ID NO:3:  
85  
86 (i) SEQUENCE CHARACTERISTICS:  
87 (A) LENGTH: 45 base pairs  
88 (B) TYPE: nucleic acid  
89 (C) STRANDEDNESS: single  
90 (D) TOPOLOGY: linear  
91  
92 (ii) MOLECULE TYPE: DNA  
93  
94 (ix) FEATURE:  
95 (A) NAME/KEY: CDS  
96 (B) LOCATION: 1..45  
97  
98 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
99

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100 TCT GTT AAG AAG TAT TAT ATC CAT GGT AAG TTT ACT ATA CTT TAG 45  
101 Ser Val Lys Lys Tyr Tyr Ile His Gly Lys Phe Thr Ile Leu \*  
102 1 5 10 15  
103  
104

## 105 (2) INFORMATION FOR SEQ ID NO:4:

106  
107 (i) SEQUENCE CHARACTERISTICS:  
108 (A) LENGTH: 14 amino acids  
109 (B) TYPE: amino acid  
110 (D) TOPOLOGY: linear  
111

112 (ii) MOLECULE TYPE: protein

113  
114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

115  
116 Ser Val Lys Lys Tyr Tyr Ile His Gly Lys Phe Thr Ile Leu  
117 1 5 10 15  
118  
119

## 120 (2) INFORMATION FOR SEQ ID NO:5:

121  
122 (i) SEQUENCE CHARACTERISTICS:  
123 (A) LENGTH: 27 base pairs  
124 (B) TYPE: nucleic acid  
125 (C) STRANDEDNESS: single  
126 (D) TOPOLOGY: linear  
127

128 (ii) MOLECULE TYPE: DNA

129  
130  
131 (ix) FEATURE:

132 (A) NAME/KEY: CDS  
133 (B) LOCATION: 1..27  
134

135 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

136  
137 GGT ATG TGT ACT GTA CTT TTC ATG GAT 27  
138 Gly Met Cys Thr Val Leu Phe Met Asp  
139 1 5  
140  
141

## 142 (2) INFORMATION FOR SEQ ID NO:6:

143  
144 (i) SEQUENCE CHARACTERISTICS:  
145 (A) LENGTH: 9 amino acids  
146 (B) TYPE: amino acid  
147 (D) TOPOLOGY: linear  
148

149 (ii) MOLECULE TYPE: protein

150  
151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

152

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153 Gly Met Cys Thr Val Leu Phe Met Asp  
154 1 5  
155  
156

157 (2) INFORMATION FOR SEQ ID NO:7:  
158

159 (i) SEQUENCE CHARACTERISTICS:  
160 (A) LENGTH: 18 base pairs  
161 (B) TYPE: nucleic acid  
162 (C) STRANDEDNESS: single  
163 (D) TOPOLOGY: linear  
164

165 (ii) MOLECULE TYPE: DNA  
166

167 (ix) FEATURE:  
168 (A) NAME/KEY: CDS  
169 (B) LOCATION: 1..18  
170

171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
172

173 GGT AAG TTT ACT ATA CTT  
174 Gly Lys Phe Thr Ile Leu  
175 10 15  
176  
177  
178

18

179 (2) INFORMATION FOR SEQ ID NO:8:  
180

181 (i) SEQUENCE CHARACTERISTICS:  
182 (A) LENGTH: 6 amino acids  
183 (B) TYPE: amino acid  
184 (D) TOPOLOGY: linear  
185

186 (ii) MOLECULE TYPE: protein  
187188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
189

190 Gly Lys Phe Thr Ile Leu  
191 1 5  
192  
193  
194

195 (2) INFORMATION FOR SEQ ID NO:9:  
196

197 (i) SEQUENCE CHARACTERISTICS:  
198 (A) LENGTH: 2415 base pairs  
199 (B) TYPE: nucleic acid  
200 (C) STRANDEDNESS: single  
201 (D) TOPOLOGY: linear  
202

203 (ii) MOLECULE TYPE: DNA  
204

205 (ix) FEATURE:

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206      (A) NAME/KEY: CDS
207      (B) LOCATION: 1..2415
208
209      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
210
211      ATG  ATT  TGT  CAA  AAA  TTC  TGT  GTG  GTT  TTG  TTA  CAT  TGG  GAA  TTT  ATT      48
212      Met  Ile  Cys  Gln  Lys  Phe  Cys  Val  Val  Leu  Leu  His  Trp  Glu  Phe  Ile
213      1          5          10          15
214
215      TAT  GTG  ATA  ACT  GCG  TTT  AAC  TTG  TCA  TAT  CCA  ATT  ACT  CCT  TGG  AGA      96
216      Tyr  Val  Ile  Thr  Ala  Phe  Asn  Leu  Ser  Tyr  Pro  Ile  Thr  Pro  Trp  Arg
217      20          25          30
218
219      TTT  AAG  TTG  TCT  TGC  ATG  CCA  CCA  AAT  TCA  ACC  TAT  GAC  TAC  TTC  CTT      144
220      Phe  Lys  Leu  Ser  Cys  Met  Pro  Pro  Asn  Ser  Thr  Tyr  Asp  Tyr  Phe  Leu
221      35          40          45
222
223      TTG  CCT  GCT  GGA  CTC  TCA  AAG  AAT  ACT  TCA  AAT  TCG  AAT  GGA  CAT  TAT      192
224      Leu  Pro  Ala  Gly  Leu  Ser  Lys  Asn  Thr  Ser  Asn  Ser  Asn  Gly  His  Tyr
225      50          55          60
226
227      GAG  ACA  GCT  GTT  GAA  CCT  AAG  TTT  AAT  TCA  AGT  GGT  ACT  CAC  TTT  TCT      240
228      Glu  Thr  Ala  Val  Glu  Pro  Lys  Phe  Asn  Ser  Ser  Gly  Thr  His  Phe  Ser
229      65          70          75          80
230
231      AAC  TTA  TCC  AAA  ACA  ACT  TTC  CAC  TGT  TGC  TTT  CGG  AGT  GAG  CAA  GAT      288
232      Asn  Leu  Ser  Lys  Thr  Thr  Phe  His  Cys  Cys  Phe  Arg  Ser  Glu  Gln  Asp
233      85          90          95
234
235      AGA  AAC  TGC  TCC  TTA  TGT  GCA  GAC  AAC  ATT  GAA  GGA  AAG  ACA  TTT  GTT      336
236      Arg  Asn  Cys  Ser  Leu  Cys  Ala  Asp  Asn  Ile  Glu  Gly  Lys  Thr  Phe  Val
237      100          105          110
238
239      TCA  ACA  GTA  AAT  TCT  TTA  GTT  TTT  CAA  CAA  ATA  GAT  GCA  AAC  TGG  AAC      384
240      Ser  Thr  Val  Asn  Ser  Leu  Val  Phe  Gln  Gln  Ile  Asp  Ala  Asn  Trp  Asn
241      115          120          125
242
243      ATA  CAG  TGC  TGG  CTA  AAA  GGA  GAC  TTA  AAA  TTA  TTC  ATC  TGT  TAT  GTG      432
244      Ile  Gln  Cys  Trp  Leu  Lys  Gly  Asp  Leu  Lys  Leu  Phe  Ile  Cys  Tyr  Val
245      130          135          140
246
247      GAG  TCA  TTA  TTT  AAG  AAT  CTA  TTC  AGG  AAT  TAT  AAC  TAT  AAG  GTC  CAT      480
248      Glu  Ser  Leu  Phe  Lys  Asn  Leu  Phe  Arg  Asn  Tyr  Asn  Tyr  Lys  Val  His
249      145          150          155          160
250
251      CTT  TTA  TAT  GTT  CTG  CCT  GAA  GTG  TTA  GAA  GAT  TCA  CCT  CTG  GTT  CCC      528
252      Leu  Leu  Tyr  Val  Leu  Pro  Glu  Val  Leu  Glu  Asp  Ser  Pro  Leu  Val  Pro
253      165          170          175
254
255      CAA  AAA  GGC  AGT  TTT  CAG  ATG  GTT  CAC  TGC  AAT  TGC  AGT  GTT  CAT  GAA      576
256      Gln  Lys  Gly  Ser  Phe  Gln  Met  Val  His  Cys  Asn  Cys  Ser  Val  His  Glu
257      180          185          190
258

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**SEQUENCE VERIFICATION REPORT**  
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Line	Error	Original Text
80	Stop Codon at end of sequence removed - no error	
116	Stop Codon at end of sequence removed - no error	
577	Stop Codon at end of sequence removed - no error	